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RAW SEQUENCE LISTING DATE: 12/11/2000
 PATENT APPLICATION: US/09/603,208A TIME: 19:47:08

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\12112000\I603208A.raw

3 <110> APPLICANT: Pompejus, Markus
 4 Kroger, Burkhard
 5 Schroder, Hartwig
 6 Zelder, Oskar
 7 Haberhauer, Gregor
 8 Lee, Heung-Shick
 9 Kim, Hyung-Joon
 11 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
 12 RESISTANCE AND TOLERANCE PROTEINS
 14 <130> FILE REFERENCE: BGI-124CP
 16 <140> CURRENT APPLICATION NUMBER: 09/603,208A
 17 <141> CURRENT FILING DATE: 2000-06-23
 19 <150> PRIOR APPLICATION NUMBER: 60/141031
 20 <151> PRIOR FILING DATE: 1999-06-25
 22 <150> PRIOR APPLICATION NUMBER: 60/142692
 23 <151> PRIOR FILING DATE: 1999-07-01
 25 <150> PRIOR APPLICATION NUMBER: 60/151214
 26 <151> PRIOR FILING DATE: 1999-08-27
 28 <150> PRIOR APPLICATION NUMBER: DE 19930429.7
 29 <151> PRIOR FILING DATE: 1999-07-01
 31 <150> PRIOR APPLICATION NUMBER: DE 19931413.6
 32 <151> PRIOR FILING DATE: 1999-07-08
 34 <150> PRIOR APPLICATION NUMBER: DE 19931457.8
 35 <151> PRIOR FILING DATE: 1999-07-08
 37 <150> PRIOR APPLICATION NUMBER: DE 19931541.8
 38 <151> PRIOR FILING DATE: 1999-07-08
 40 <150> PRIOR APPLICATION NUMBER: DE 19932209.0
 41 <151> PRIOR FILING DATE: 1999-07-09
 43 <150> PRIOR APPLICATION NUMBER: DE 19932230.9
 44 <151> PRIOR FILING DATE: 1999-07-09
 46 <150> PRIOR APPLICATION NUMBER: DE 19932914.1
 47 <151> PRIOR FILING DATE: 1999-07-14
 49 <150> PRIOR APPLICATION NUMBER: DE 19940764.9
 50 <151> PRIOR FILING DATE: 1999-08-27
 52 <150> PRIOR APPLICATION NUMBER: DE 19941382.7
 53 <151> PRIOR FILING DATE: 1999-08-31
 55 <160> NUMBER OF SEQ ID NOS: 306
 57 <210> SEQ ID NO: 1
 58 <211> LENGTH: 1566
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Corynebacterium glutamicum
 62 <220> FEATURE:
 63 <221> NAME/KEY: CDS
 64 <222> LOCATION: (101)..(1543)
 65 <223> OTHER INFORMATION: RXA01524
 67 <400> SEQUENCE: 1
 68 ttgtggcact ctttagtagt tttttctcat agctcagttt cgcaacttta gagaactcta 60

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70 gaaactgagc ttcattgctgt gaaaggcctt ttctccattc atg gat tcc caa att 115
71                                     Met Asp Ser Gln Ile
72                                     1         5
74 aat act cag acc tct ccg gca gct gcg aag ctg cct agg gag gtc gtt 163
75 Asn Thr Gln Thr Ser Pro Ala Ala Ala Lys Leu Pro Arg Glu Val Val
76                                     10        15        20
78 gtt gtt ctt tcg atc ctc gtg gtt tcc gcg atg atc atg att ctt aat 211
79 Val Val Leu Ser Ile Leu Val Val Ser Ala Met Ile Met Ile Leu Asn
80                                     25        30        35
82 gaa acc att ctg tcg gtt gcg ttg cct tcc atc atg gaa gat ttc tcc 259
83 Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile Met Glu Asp Phe Ser
84                                     40        45        50
86 gtg cct gaa act act gca cag tgg ttg acc act ggc ttt atg ttg acg 307
87 Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr Gly Phe Met Leu Thr
88                                     55        60        65
90 atg gca gtg gtg att cca act act ggt tat ctg ctt gat cgt ttt tcc 355
91 Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu Leu Asp Arg Phe Ser
92 70                                     75        80        85
94 act aag acg atc ttt gtt act gcg ttg ttg ttc ttt acg gtt ggt acg 403
95 Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe Phe Thr Val Gly Thr
96                                     90        95       100
98 ttg act gcg gcg ttg gct cca acg ttt gcg gtg ctg ctt ggt gct cgt 451
99 Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val Leu Leu Gly Ala Arg
100                                     105       110       115
102 atc gtt cag gcg gtt ggt act gcg ctg gtg atg cct ttg ctg atg acg 499
103 Ile Val Gln Ala Val Gly Thr Ala Leu Val Met Pro Leu Leu Met Thr
104                                     120       125       130
106 gtt acg ttg acg gtg gtt cct gcg gag cgt cgt ggt tcg atg atg ggc 547
107 Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg Gly Ser Met Met Gly
108                                     135       140       145
110 att att tcc atc gtg att tct gtt gcg ccg gcg ctt ggt cct acg ttg 595
111 Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala Leu Gly Pro Thr Leu
112 150                                     155       160       165
114 tct ggt gtc att ctt aac tct ttg acc tgg cac tgg ttg ttt tgg atg 643
115 Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His Trp Leu Phe Trp Met
116                                     170       175       180
118 atg ctt ccg atc gtt gtt atc gct ttg gta att ggt ttc ttc ttg atc 691
119 Met Leu Pro Ile Val Val Ile Ala Leu Val Ile Gly Phe Phe Leu Ile
120                                     185       190       195
122 aaa aat atc ggc gaa acc aag atc acc cca ctg gat gtt ctg tct gtc 739
123 Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu Asp Val Leu Ser Val
124                                     200       205       210
126 atc ctt tcg gtg ttt gcc ttc ggt ttg gtg tac ggc ttc agt tcc 787
127 Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val Tyr Gly Phe Ser Ser
128                                     215       220       225
130 ttc gga gca atc ctg gag ggc gaa ggc acc gta ggt atc ttc gcg atc 835
131 Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val Gly Ile Phe Ala Ile
132 230                                     235       240       245
134 gtc gtt ggc gcc atc gca ctc ctc atc ttt gct ttg cga cag cac caa 883

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135 Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala Leu Arg Gln His Gln
136          250          255          260
138 ctc ggc aag caa gac aaa gca ctg atg qat ctc cga gcc ttc aag gtg 931
139 Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu Arg Ala Phe Lys Val
140          265          270          275
142 agg aac ttc agc ttc tcc ttg acc acc atc ctt ttg gcg ttc ggc gcg 979
143 Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu Leu Ala Phe Gly Ala
144          280          285          290
146 atg ctc gga acc gtc atg gtt ttg cca atc tac ctg cag act tcc ctc 1027
147 Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr Leu Gln Thr Ser Leu
148          295          300          305
150 gga gtt act gct ttg gtg acc ggt ttg gtt gtt atg ccc ggc ggc ctc 1075
151 Gly Val Thr Ala Leu Val Thr Gly Leu Val Val Met Pro Gly Gly Leu
152 310          315          320          325
154 ctc cag ggt ctg atc agc cca ttc atc gga cyt ttc tac gac aag gtc 1123
155 Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg Phe Tyr Asp Lys Val
156          330          335          340
158 ggt cca cgt ccg ctg ctg att ccc gga gca att gcg ctg gct atc gcg 1171
159 Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile Ala Leu Ala Ile Ala
160          345          350          355
162 gca tcc tcg atg act ttt ctc aat gag aat tca ccc gtg tgg atg gtc 1219
163 Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser Pro Val Trp Met Val
164          360          365          370
166 gtg gtc atg cac gtt gtg ttc agc atc ggc atg tgt ttg atg atg acc 1267
167 Val Val Met His Val Val Phe Ser Ile Gly Met Cys Leu Met Met Thr
168          375          380          385
170 cct ctc atg acc acc gct ctc ggc gcc ctt ccg aag cac ctc tat ggt 1315
171 Pro Leu Met Thr Thr Ala Leu Gly Ala Leu Pro Lys His Leu Tyr Gly
172 390          395          400          405
174 cac ggc tcc gca att ttg aac acg ttc caa cag ctc gca ggc gca gcc 1363
175 His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln Leu Ala Gly Ala Ala
176          410          415          420
178 gga aca gcg atc atg att gca gca ctt tcc ttc ggc act tcc att gca 1411
179 Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe Gly Thr Ser Ile Ala
180          425          430          435
182 gcg tct tcg gga tct gcg cat gct gaa gct gtt gcc gct ggt acc aag 1459
183 Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val Ala Ala Gly Thr Lys
184          440          445          450
186 gtt gcg ttc atc gca ggc gca atc atc gcg gtg atc gct ttg gtt gtt 1507
187 Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val Ile Ala Leu Val Val
188          455          460          465
190 tcc ctc ttc gtc act cgc gtc gag gaa gaa gct cac taaataccaaa 1553
191 Ser Leu Phe Val Thr Arg Val Glu Gln Glu Ala His
192 470          475          480
194 aaaatggggc aga 1566
197 <210> SEQ ID NO: 2
198 <211> LENGTH: 481
199 <212> TYPE: PRT
200 <213> ORGANISM: Corynebacterium glutamicum

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RAW SEQUENCE LISTING DATE: 12/11/2000
 PATENT APPLICATION: US/09/603,208A TIME: 19:47:08

Input Set : A:\Pto.amc
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202 <400> SEQUENCE: 2
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204 1 5 10 15
206 Pro Arg Glu Val Val Val Val Leu Ser Ile Leu Val Val Ser Ala Met
207 20 25 30
209 Ile Met Ile Leu Asn Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile
210 35 40 45
212 Met Glu Asp Phe Ser Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr
213 50 55 60
215 Gly Phe Met Leu Thr Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu
216 65 70 75 80
218 Leu Asp Arg Phe Ser Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe
219 85 90 95
221 Phe Thr Val Gly Thr Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val
222 100 105 110
224 Leu Leu Gly Ala Arg Ile Val Gln Ala Val Gly Thr Ala Leu Val Met
225 115 120 125
227 Pro Leu Leu Met Thr Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg
228 130 135 140
230 Gly Ser Met Met Gly Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala
231 145 150 155 160
233 Leu Gly Pro Thr Leu Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His
234 165 170 175
236 Trp Leu Phe Trp Met Met Leu Pro Ile Val Val Ile Ala Leu Val Ile
237 180 185 190
239 Gly Phe Phe Leu Ile Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu
240 195 200 205
242 Asp Val Leu Ser Val Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val
243 210 215 220
245 Tyr Gly Phe Ser Ser Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val
246 225 230 235 240
248 Gly Ile Phe Ala Ile Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala
249 245 250 255
251 Leu Arg Gln His Gln Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu
252 260 265 270
254 Arg Ala Phe Lys Val Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu
255 275 280 285
257 Leu Ala Phe Gly Ala Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr
258 290 295 300
260 Leu Gln Thr Ser Leu Gly Val Thr Ala Leu Val Thr Gly Leu Val Val
261 305 310 315 320
263 Met Pro Gly Gly Leu Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg
264 325 330 335
266 Phe Tyr Asp Lys Val Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile
267 340 345 350
269 Ala Leu Ala Ile Ala Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser
270 355 360 365
272 Pro Val Trp Met Val Val Val Met His Val Val Phe Ser Ile Gly Met
273 370 375 380

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275	Cys	Leu	Met	Met	Thr	Pro	Leu	Met	Thr	Thr	Ala	Leu	Gly	Ala	Leu	Pro
276	385					390					395					400
278	Lys	His	Leu	Tyr	Gly	His	Gly	Ser	Ala	Ile	Leu	Asn	Thr	Phe	Gln	Gln
279					405					410					415	
281	Leu	Ala	Gly	Ala	Ala	Gly	Thr	Ala	Ile	Met	Ile	Ala	Ala	Leu	Ser	Phe
282				420					425					430		
284	Gly	Thr	Ser	Ile	Ala	Ala	Ser	Ser	Gly	Ser	Ala	His	Ala	Glu	Ala	Val
285			435				440						445			
287	Ala	Ala	Gly	Thr	Lys	Val	Ala	Phe	Ile	Ala	Gly	Ala	Ile	Ile	Ala	Val
288		450					455					460				
290	Ile	Ala	Leu	Val	Val	Ser	Leu	Phe	Val	Thr	Arg	Val	Glu	Glu	Glu	Ala
291	465					470					475					480
293	His															
297	<210> SEQ ID NO: 3															
298	<211> LENGTH: 371															
299	<212> TYPE: DNA															
300	<213> ORGANISM: Corynebacterium glutamicum															
302	<220> FEATURE:															
303	<221> NAME/KEY: CDS															
304	<222> LOCATION: (52)..(348)															
305	<223> OTHER INFORMATION: RXA00497															
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309								Val Ala								
310								1								
312	aac	gtc	aac	atc	aag	ccg	ctt	gag	gac	aag	atc	ctc	ggt	cag	atc	aac
313	Asn	Val	Asn	Ile	Lys	Pro	Leu	Glu	Asp	Lys	Ile	Leu	Val	Gln	Ile	Asn
314			5					10					15			
316	gaa	gca	gag	acc	acc	acc	gct	tcc	ggc	ctg	gtc	att	cca	gat	tcc	gct
317	Glu	Ala	Glu	Thr	Thr	Thr	Ala	Ser	Gly	Leu	Val	Ile	Pro	Asp	Ser	Ala
318		20					25					30				
320	aag	gaa	aag	cca	caa	gag	gca	acc	gtt	atc	gca	gtt	ggc	cca	ggc	cgc
321	Lys	Glu	Lys	Pro	Gln	Glu	Ala	Thr	Val	Ile	Ala	Val	Gly	Pro	Gly	Arg
322	35					40					45				50	</

FYI:

Please Note:

Please Note: Use f n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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PATENT APPLICATION: US/09/603,208A

TIME: 19:47:09

Input Set : A:\Pto.amc

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L:3092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
 L:3093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
 L:3096 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
 L:3097 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
 L:3223 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
 L:3223 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
 L:3223 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
 L:3226 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
 L:3226 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
 M:340 Repeated in SeqNo=34
 L:4204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
 L:4212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
 L:4216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
 L:4219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
 L:4220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45
 L:4261 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
 L:4261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
 L:4261 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:46
 L:4267 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
 L:4267 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
 M:340 Repeated in SeqNo=46
 L:4270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
 L:4270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
 L:4273 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:46
 L:4273 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:46
 L:4297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
 L:4299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
 L:4300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
 L:4323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
 L:4324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
 L:4327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
 L:4341 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
 L:4341 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
 L:4341 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:48
 L:4359 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:48
 L:4359 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:48
 M:340 Repeated in SeqNo=48
 L:23699 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:302
 L:23699 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:302
 L:23699 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:302